

CRF Errors Corrected by the STIC Systems Branch

01PE #2

Serial Number: 09/818,825

CRF Processing Date: _____
 Edited by: _____
 Verified by: _____ (STIC staff)

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☒ Corrected an obvious error in the response, specifically:
<213> primer Artificial Sequence. -> deleted primer (Seq. #3)
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

***Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.**

OIPE

RAW SEQUENCE LISTING

DATE: 04/18/2001

PATENT APPLICATION: US/09/816,825

TIME: 17:32:37

Input Set : A:\Cpg.pto

Output Set: N:\CRF3\04182001\I816825.raw

4 <110> APPLICANT: Bistrup, Annette
 5 Rosen, Steven D.
 6 Hemmerich, Stefan
 8 <120> TITLE OF INVENTION: GLYCOSYL SULFOTRANSFERASE-3
 11 <130> FILE REFERENCE: 6510-107CON
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/816,825
 14 <141> CURRENT FILING DATE: 2001-03-22
 16 <150> PRIOR APPLICATION NUMBER: 09/045,284
 17 <151> PRIOR FILING DATE: 1998-03-20
 19 <160> NUMBER OF SEQ ID NOS: 9
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 2032
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
 28 <400> SEQUENCE: 1
 29 ggctcgaggc caggatgcct ccagtcctggg ggaaaatgct tcctcatttg cttctcccag 60
 30 cccacctcaa gcagtcctccc cacccttga gtctcagcag tgtaaagct gttactttca 120
 31 cagcttcctg ggagcgagtg ctttctcaag cccgtcttgc aaggtcttcc acttcagcac 180
 32 aatgctactg cctaaaaaaa tgaagctcct gctgtttctg gtttcccaga tggccatctt 240
 33 ggctctattc ttccacatgt acagccacaa catcagctcc ctgtctatga aggcacagcc 300
 34 cgagcgcatg cagtgctgg ttctgtcttc ctggcgctct ggctcttctt ttgtggggca 360
 35 gctttttggg cagcaccag atgttttcta cctgatggag cccgcctggc acgtgtggat 420
 36 gaccttcaag cagagcaccg cctggatgct gcacatggct gtgcgggac tgatacgggc 480
 37 cgtcttcttg tgcgacatga gcgtctttga tgcctacatg gaacctgggc cccggagaca 540
 38 gtccagcctc tttcagtggg agaacagccg ggcctgtgt tctgcacctg cctgtgacat 600
 39 catccacaaa gatgaaatca tccccgggc tcaactgcagg ctctgtgca gtcaacagcc 660
 40 ctttgagggtg gtggagaagg cctgccgctc ctacagccac gtggtgctca aggaggtgcg 720
 41 cttcttcaac ctgcagtcct tctaccgct gctgaaagac cctccctca acctgcata 780
 42 cgtgcacctg gtccgggacc cccgggcccgt gttccgttcc cgagaacgca caaagggaga 840
 43 tctcatgatt gacagtcgca ttgtgatggg gcagcatgag cagaaactca agaaggagga 900
 44 ccaaccctac tatgtgatgc aggtcatctg ccaaagccag ctggagatct acaagaccat 960
 45 ccagtccttg cccaaggccc tgcaggaacg ctacctgctt gtgcgctatg aggacctggc 1020
 46 tgagcctcct gtggcccaga cttcccgaat gtatgaattc gtgggatttg aattcttggc 1080
 47 ccatcttcag acctgggtgc ataacatcac ccgaggcaag ggcattgggtg accacgcttt 1140
 48 ccacacaaat gccagggatg cccttaatgt ctcccaggct tggcgctggt ctttgcccta 1200
 49 tgaaaagggt tctcgacttc agaaagcctg tggcgatgcc atgaatttgc tgggctaccg 1260
 50 ccacgtcaga tctgaacaag aacagagaaa cctgttgctg gatcttctgt ctacctggac 1320
 51 tgtccctgag caaatccact aagagggttg agaaggcttt gctgccacct ggtgtcagcc 1380
 52 tcagtcactt tctctgaatg cttctgagcc ttgacctacat ctctgacct taactacatg 1440
 53 tctgtgggta tcacactgag tgtgagttgt gtccacacgt gctcaagcag aaggactttt 1500
 54 gtgtccatgc ttgtgtctag aaaacagact ggggaacctt atgtgagcag cacatcccac 1560
 55 cagtgaacaa gggatttgc cttcttcttt tcttgatctt cctgtctggg cagacttcag 1620
 56 agactttgtg gcttgagggc ctattaagca cgacacagta tcagtggat tgatccataa 1680
 57 acctccctgt ccacatcttg cccaatgggg aatggatctt tcaccaaaga gctcaccagc 1740
 58 attttccaca gagatgcaaa ttctgagccc ttggagttcc cagtggattc aaggaaggaa 1800
 59 gtgggaacaa ggttgatgc ctacttatga gcttgacct cacagctatc ggtaatcaga 1860

RAW SEQUENCE LISTING

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Input Set : A:\Cpg.pto

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60 aatatgaaac aaaatctctg cacaaaagag caagctctta agttcacagg gtgcctgggc 1920
61 tgcatttgaa tatcacttcc cctctgcatt ttcccatcac atagaagact ttgacctgtg 1980
62 aagctgccat ctgttaatac taaaattccc aaataagaaa aaaaaaaaaa aa 2032
64 <210> SEQ ID NO: 2
65 <211> LENGTH: 386
66 <212> TYPE: PRT
67 <213> ORGANISM: Homo sapiens
69 <400> SEQUENCE: 2
70 Met Leu Leu Pro Lys Lys Met Lys Leu Leu Phe Leu Val Ser Gln
71 1 5 10 15
72 Met Ala Ile Leu Ala Leu Phe Phe His Met Tyr Ser His Asn Ile Ser
73 20 25 30
74 Ser Leu Ser Met Lys Ala Gln Pro Glu Arg Met His Val Leu Val Leu
75 35 40 45
76 Ser Ser Trp Arg Ser Gly Ser Ser Phe Val Gly Gln Leu Phe Gly Gln
77 50 55 60
78 His Pro Asp Val Phe Tyr Leu Met Glu Pro Ala Trp His Val Trp Met
79 65 70 75 80
80 Thr Phe Lys Gln Ser Thr Ala Trp Met Leu His Met Ala Val Arg Asp
81 85 90 95
82 Leu Ile Arg Ala Val Phe Leu Cys Asp Met Ser Val Phe Asp Ala Tyr
83 100 105 110
84 Met Glu Pro Gly Pro Arg Arg Gln Ser Ser Leu Phe Gln Trp Glu Asn
85 115 120 125
86 Ser Arg Ala Leu Cys Ser Ala Pro Ala Cys Asp Ile Ile Pro Gln Asp
87 130 135 140
88 Glu Ile Ile Pro Arg Ala His Cys Arg Leu Leu Cys Ser Gln Gln Pro
89 145 150 155 160
90 Phe Glu Val Val Glu Lys Ala Cys Arg Ser Tyr Ser His Val Val Leu
91 165 170 175
92 Lys Glu Val Arg Phe Phe Asn Leu Gln Ser Leu Tyr Pro Leu Leu Lys
93 180 185 190
94 Asp Pro Ser Leu Asn Leu His Ile Val His Leu Val Arg Asp Pro Arg
95 195 200 205
96 Ala Val Phe Arg Ser Arg Glu Arg Thr Lys Gly Asp Leu Met Ile Asp
97 210 215 220
98 Ser Arg Ile Val Met Gly Gln His Glu Gln Lys Leu Lys Lys Glu Asp
99 225 230 235 240
100 Gln Pro Tyr Tyr Val Met Gln Val Ile Cys Gln Ser Gln Leu Glu Ile
101 245 250 255
102 Tyr Lys Thr Ile Gln Ser Leu Pro Lys Ala Leu Gln Glu Arg Tyr Leu
103 260 265 270
104 Leu Val Arg Tyr Glu Asp Leu Ala Arg Ala Pro Val Ala Gln Thr Ser
105 275 280 285
106 Arg Met Tyr Glu Phe Val Gly Leu Glu Phe Leu Pro His Leu Gln Thr
107 290 295 300
108 Trp Val His Asn Ile Thr Arg Gly Lys Gly Met Gly Asp His Ala Phe
109 305 310 315 320
110 His Thr Asn Ala Arg Asp Ala Leu Asn Val Ser Gln Ala Trp Arg Trp

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111          325          330          335
112 Ser Leu Pro Tyr Glu Lys Val Ser Arg Leu Gln Lys Ala Cys Gly Asp
113          340          345          350
114 Ala Met Asn Leu Leu Gly Tyr Arg His Val Arg Ser Glu Gln Glu Gln
115          355          360          365
116 Arg Asn Leu Leu Leu Asp Leu Leu Ser Thr Trp Thr Val Pro Glu Gln
117          370          375          380
118 Ile His
119 385

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121 <210> SEQ ID NO: 3

122 <211> LENGTH: 29

123 <212> TYPE: DNA

124 <213> ORGANISM: Artificial Sequence

126 <220> FEATURE:

127 <223> OTHER INFORMATION: primer

129 <221> NAME/KEY: misc_feature

130 <222> LOCATION: (0)...(0)

131 <223> OTHER INFORMATION: n=inosine

133 <400> SEQUENCE: 3

W--> 134 twytwycnt wygarccnct ntggcayst

29

136 <210> SEQ ID NO: 4

137 <211> LENGTH: 29

138 <212> TYPE: DNA

139 <213> ORGANISM: Artificial Sequence

141 <220> FEATURE:

142 <223> OTHER INFORMATION: primer

144 <221> NAME/KEY: misc_feature

145 <222> LOCATION: (0)...(0)

146 <223> OTHER INFORMATION: n=inosine

148 <400> SEQUENCE: 4

W--> 149 ctnaancnts tncwrctnst nmgnraycc

29

151 <210> SEQ ID NO: 5

152 <211> LENGTH: 29

153 <212> TYPE: DNA

154 <213> ORGANISM: Artificial Sequence

156 <220> FEATURE:

157 <223> OTHER INFORMATION: primer

159 <221> NAME/KEY: misc_feature

160 <222> LOCATION: (0)...(0)

161 <223> OTHER INFORMATION: n=inosine

163 <400> SEQUENCE: 5

W--> 164 ggrtyncna snagywgnas nagnttnag

29

166 <210> SEQ ID NO: 6

167 <211> LENGTH: 26

168 <212> TYPE: DNA

169 <213> ORGANISM: Artificial Sequence

171 <220> FEATURE:

172 <223> OTHER INFORMATION: primer

174 <221> NAME/KEY: misc_feature

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175 <222> LOCATION: (0)...(0)
176 <223> OTHER INFORMATION: n=inosine
178 <400> SEQUENCE: 6
W--> 179 agrtcytcrt ancknagnag nakrta                                26
181 <210> SEQ ID NO: 7
182 <211> LENGTH: 37
183 <212> TYPE: DNA
184 <213> ORGANISM: Homo sapiens
186 <400> SEQUENCE: 7
187 aaactcaaga aggaggacca accctactat gtgatgc                                37
189 <210> SEQ ID NO: 8
190 <211> LENGTH: 47
191 <212> TYPE: DNA
192 <213> ORGANISM: Homo sapiens
194 <400> SEQUENCE: 8
195 ataaagcttg tggatttggt cagggacatt ccaggtagac agaagat                    47
197 <210> SEQ ID NO: 9
198 <211> LENGTH: 6
199 <212> TYPE: PRT
200 <213> ORGANISM: Homo sapiens
202 <400> SEQUENCE: 9
203 Val Arg Tyr Glu Asp Leu
204 1                               5

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VERIFICATION SUMMARY

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Input Set : A:\Cpg.pto

Output Set: N:\CRF3\04182001\I816825.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number

L:134 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:149 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4

L:164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

L:179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6